

SEQUENCE LISTING



5 <110> Lethé, Bernard
Lucas, Sophie
De Smet, Charles
Godelaine, Daniele
Boon-Falleur, Thierry

10 <120> LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS

<130> L0461/7066

15 <140> US 09/341,829
<141> 1999-10-18

<150> US 08/791,495
<151> 1997-01-27

20 <150> PCT/US98/01445
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gcccctcaca tttagccgac tgactgtctgc agaccaccgc caactgcagc tctccatcag 180
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TECH CENTER 1600/2900

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 1 5 10 15

10 gat ggc cca gga ggc cct ggc att cct gat ggc cca ggg ggc aat gct 157
 Asp Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala
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ggc ggc cca gga gag ggc ggt gcc acg ggc ggc aga ggt ccc cgg ggc 205
 Gly Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly
 35 40 45

15 gca ggg gca gca agg gcc tcg ggg ccg aga gga ggc gcc ccg cgg ggt 253
 Ala Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly
 50 55 60

20 ccg cat ggc ggt gcc gct tct gcg cag gat gga agg tgc ccc tgc ggg 301
 Pro His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly
 65 70 75

25 gcc agg agg ccg gac agc cgc ctg ctt cag ttg cac atc acg atg cct 349
 Ala Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro
 80 85 90 95

30 ttc tcg tcg ccc atg gaa gcg gag ctg gtc cgc agg atc ctg tcc cgg 397
 Phe Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg
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gat gcc gca cct ctc ccc cga cca ggg gcg gtt ctg aag gac ttc acc 445
 Asp Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr
 115 120 125

35 gtg tcc ggc aac cta ctg ttt atg tca gtt cgg gac cag gac agg gaa 493
 Val Ser Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu
 130 135 140

40 ggc gct ggg cgg atg agg gtg gtg ggt tgg ggg ctg gga tcc gcc tcc 541
 Gly Ala Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser
 145 150 155

45 ccg gag ggg cag aaa gct aga gat ctc aga aca ccc aaa cac aag gtc 589
 Pro Glu Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val
 160 165 170 175

tca gaa cag aga cct ggt aca cca ggc ccg ccg cca ccc gag gga gcc 637
 Ser Glu Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala
 180 185 190

50 cag gga gat ggg tgc aga ggt gtc gcc ttt aat gtg atg ttc tct gcc 685
 Gln Gly Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala
 195 200 205

55 cct cac att tagccgactg actgctgcag accaccgcca actgcagctc 734
 Pro His Ile
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60 tccatcagct cctgtctcca gcagctttcc ctggttgatgt ggatcacgca gtgctttctg 794
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 15 35 40 45
 Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
 50 55 60
 His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
 20 65 70 75 80
 Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe
 85 90 95
 Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp
 100 105 110
 Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val
 115 120 125
 Ser Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly
 130 135 140
 Ala Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro
 145 150 155 160
 Glu Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser
 165 170 175
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 180 185 190
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 His Ile
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Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly
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cca gga ggc cct ggc att cct gat ggc cca ggg ggc aat gct ggc ggc 151
5 Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly
20 25 30

cca gga gag gcg ggt gcc acg ggc ggc aga ggt ccc cgg ggc gca ggg 199
10 Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly
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gca gca agg gcc tcg ggg ccg aga gga ggc gcc ccg cgg ggt ccg cat 247
15 Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His
50 55 60 65

ggc ggt gcc gct tct gcg cag gat gga agg tgc ccc tgc ggg gcc agg 295
Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg
70 75 80

agg ccg gac agc cgc ctg ctt cag ttg cac atc acg atg cct ttc tcg 343
20 Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser
85 90 95

tcg ccc atg gaa gcg gag ctg gtc cgc agg atc ctg tcc cgg gat gcc 391
25 Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala
100 105 110

gca cct ctc ccc cga cca ggg gcg gtt ctg aag gac ttc acc gtg tcc 439
30 Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser
115 120 125

ggc aac cta ctg ttt atc cga ctg act gct gca gac cac cgc caa ctg 487
35 Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu
130 135 140 145

cag ctc tcc atc agc tcc tgt ctc cag cag ctt tcc ctg ttg atg tgg 535
Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp
150 155 160

atc acg cag tgc ttt ctg ccc gtg ttt ttg gct cag gct ccc tca ggg 583
40 Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser Gly
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45 Gln Arg Arg
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Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
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Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
60 50 55 60

His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
 65 70 75 80
 5 Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe
 85 90 95
 Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp
 100 105 110
 10 Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val
 115 120 125
 Ser Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln
 130 135 140
 15 Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
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 Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly Pro
 5 10 15
 45 gga ggc cct ggc att cct gat ggc cca ggg ggc aat gct ggc ggc cca 152
 Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly Pro
 20 25 30
 50 gga gag gcg ggt gcc acg ggc ggc aga ggt ccc cgg ggc gca ggg gca 200
 Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly Ala
 35 40 45 50
 55 gca agg gcc tcg ggg ccg gga gga ggc gcc ccg cgg ggt ccg cat ggc 248
 Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro His Gly
 55 60 65
 ggc gcg gct tca ggg ctg aat gga tgc tgc aga tgc ggg gcc agg ggg 296
 Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala Arg Gly
 70 75 80
 60 ccg gag agc cgc ctg ctt gag ttc tac ctc gcc atg cct ttc gcg aca 344
 Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe Ala Thr
 85 90 95
 65 ccc atg gaa gca gag ctg gcc cgc agg agc ctg gcc cag gat gcc cca 392

Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp Ala Pro
100 105 110

5 ccg ctt ccc gtg cca ggg gtg ctt ctg aag gag ttc act gtg tcc ggc 440
Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val Ser Gly
115 120 125 130

10 aac ata ctg act atc cga ctg act gct gca gac cac cgc caa ctg cag 488
Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu Gln
135 140 145

15 ctc tcc atc agc tcc tgt ctc cag cag ctt tcc ctg ttg atg tgg atc 536
Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp Ile
150 155 160

acg cag tgc ttt ctg ccc gtg ttt ttg gct cag cct ccc tca ggg cag 584
Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly Gln
165 170 175

20 agg cgc taagcccagc ctggcgcccc ttcttaggtc atgcctcctc ccctagggaa 640
Arg Arg
180

25 tgggtcccagc acgagtggcc agttcattgt gggggcctga ttgtttgtcg ctggaggagg 700
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40 Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45

45 Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
50 55 60

His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
65 70 75 80

50 Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
85 90 95

Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
100 105 110

55 Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
115 120 125

60 Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
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Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
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Gly Gln Arg Arg
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